

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/90/556A

CRF Processing Date: 4/9/2002
 Edited by: Ar
 Verified by: Ar (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



RAW SEQUENCE LISTING

DATE: 04/09/2002

PATENT APPLICATION: US/09/901,556A

TIME: 17:34:37

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04092002\I901556A.raw

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3 <110> APPLICANT: Hotten, Gertrud
4      Neidhardt, Helge
5      Bechtold, Rolf
6      Pohl, Jens
8 <120> TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B FAMILY
10 <130> FILE REFERENCE: 100564-09021
12 <140> CURRENT APPLICATION NUMBER: 09/901,556A
13 <141> CURRENT FILING DATE: 1999-08-25
15 <150> PRIOR APPLICATION NUMBER: 08/289,222
16 <151> PRIOR FILING DATE: 1994-08-12
18 <150> PRIOR APPLICATION NUMBER: DE P 44 23 190.3
19 <151> PRIOR FILING DATE: 1994-07-01
21 <150> PRIOR APPLICATION NUMBER: EPO 92102324.8
22 <151> PRIOR FILING DATE: 1992-02-12
24 <150> PRIOR APPLICATION NUMBER: PCT/EP93/00350
25 <151> PRIOR FILING DATE: 1993-02-12
27 <160> NUMBER OF SEQ ID NOS: 53
29 <170> SOFTWARE: PatentIn version 3.1
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34 <213> ORGANISM: Homo sapiens
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71 cctggagccc acgaatcatg cagtcattca gaccctgatg aactccatgg accccgagtc 1080
73 cacaccaccc acctgctgtg tgccccacgc gctgagtgcc atcagcatcc tcttcattga 1140
75 ctctgccaac aacgtggtgt ataagcagta tgaggacatg gtcgtggagt cgtgtggctg 1200

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83 <213> ORGANISM: Homo sapiens
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90 cccagcaatg acctcctcat tcttctggc ctttctctc ctggctccaa ccacagtggc 180
92 cactcccaga gctggcggtc agtgctcagc atgtgggggg cccaccttg aactggagag 240
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164 <211> LENGTH: 401
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 3

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174 Ala Thr Ala Arg Thr Val Thr Pro Lys Gly Gln Leu Pro Gly Gly Lys
175 20 25 30
178 Ala Pro Pro Lys Ala Gly Ser Val Pro Ser Ser Phe Leu Lys Lys
179 35 40 45
182 Ala Arg Glu Pro Gly Pro Pro Arg Glu Pro Lys Glu Pro Phe Arg Pro
183 50 55 60
186 Pro Pro Ile Thr Pro His Glu Tyr Met Leu Ser Leu Tyr Arg Thr Leu
187 65 70 75 80
190 Ser Asp Ala Asp Arg Lys Gly Gly Asn Ser Ser Val Lys Leu Glu Ala
191 85 90 95
194 Gly Leu Ala Asn Thr Ile Thr Ser Phe Ile Asp Lys Gly Gln Asp Asp
195 100 105 110
198 Arg Gly Pro Val Val Arg Lys Gln Arg Tyr Val Phe Asp Ile Ser Ala
199 115 120 125
202 Leu Glu Lys Asp Gly Leu Leu Gly Ala Glu Leu Arg Ile Leu Arg Lys
203 130 135 140
206 Lys Pro Ser Asp Thr Ala Lys Pro Ala Ala Pro Gly Gly Gly Arg Ala
207 145 150 155 160
210 Ala Gln Leu Lys Leu Ser Ser Cys Pro Ser Gly Arg Gln Pro Ala Ser
211 165 170 175
214 Leu Leu Asp Val Arg Ser Val Pro Gly Leu Asp Gly Ser Gly Trp Glu
215 180 185 190
218 Val Phe Asp Ile Trp Lys Leu Phe Arg Asn Phe Lys Asn Ser Ala Gln
219 195 200 205
222 Leu Cys Leu Glu Leu Glu Ala Trp Glu Arg Gly Arg Ala Val Asp Leu
223 210 215 220
226 Arg Gly Leu Gly Phe Asp Arg Ala Ala Arg Gln Val His Glu Lys Ala
227 225 230 235 240
230 Leu Phe Leu Val Phe Gly Arg Thr Lys Lys Arg Asp Leu Phe Phe Asn
231 245 250 255
234 Glu Ile Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr Val Tyr Glu Tyr
235 260 265 270
238 Leu Phe Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu Ala Thr Arg Gln
239 275 280 285
242 Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala
243 290 295 300
246 Leu His Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile Ile Ala
247 305 310 315 320
250 Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Leu Cys Glu Phe Pro
251 325 330 335
254 Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val Ile Gln Thr Leu
255 340 345 350
258 Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys Val Pro
259 355 360 365
262 Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp Ser Ala Asn Asn
263 370 375 380
266 Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu Ser Cys Gly Cys

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275 <211> LENGTH: 352
276 <212> TYPE: PRT
277 <213> ORGANISM: Homo sapiens
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286                      20                      25                      30
289 Thr Leu Glu Leu Glu Ser Gln Arg Glu Leu Leu Leu Asp Leu Ala Lys
290                      35                      40                      45
293 Arg Ser Ile Leu Asp Lys Leu His Leu Thr Gln Arg Pro Thr Leu Asn
294                      50                      55                      60
297 Arg Pro Val Ser Arg Ala Ala Leu Arg Thr Ala Leu Gln His Leu His
298 65                      70                      75                      80
301 Gly Val Pro Gln Gly Ala Leu Leu Glu Asp Asn Arg Glu Gln Glu Cys
302                      85                      90                      95
305 Glu Ile Ile Ser Phe Ala Glu Thr Gly Leu Ser Thr Ile Asn Gln Thr
306                      100                     105                     110
309 Arg Leu Asp Phe His Phe Ser Ser Asp Arg Thr Ala Gly Asp Arg Glu
310                      115                     120                     125
313 Val Gln Gln Ala Ser Leu Met Phe Phe Val Gln Leu Pro Ser Asn Thr
314                      130                     135                     140
317 Thr Trp Thr Leu Lys Val Arg Val Leu Val Leu Gly Pro His Asn Thr
318 145                      150                     155                     160
321 Asn Leu Thr Leu Ala Thr Gln Tyr Leu Leu Glu Val Asp Ala Ser Gly
322                      165                     170                     175
325 Trp His Gln Leu Pro Leu Gly Pro Glu Ala Gln Ala Ala Cys Ser Gln
326                      180                     185                     190
329 Gly His Leu Thr Leu Glu Leu Val Leu Glu Gly Gln Val Ala Gln Ser
330                      195                     200                     205
333 Ser Val Ile Leu Gly Gly Ala Ala His Arg Pro Phe Val Ala Ala Arg
334                      210                     215                     220
337 Val Arg Val Gly Gly Lys His Gln Ile His Arg Arg Gly Ile Asp Cys
338 225                      230                     235                     240
341 Gln Gly Gly Ser Arg Met Cys Cys Arg Gln Glu Phe Phe Val Asp Phe
342                      245                     250                     255
345 Arg Glu Ile Gly Trp His Asp Trp Ile Ile Gln Pro Glu Gly Tyr Ala
346                      260                     265                     270
349 Met Asn Phe Cys Ile Gly Gln Cys Pro Leu His Ile Ala Gly Met Pro
350                      275                     280                     285
353 Gly Ile Ala Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala
354                      290                     295                     300
357 Asn Thr Ala Ala Gly Thr Thr Gly Gly Gly Ser Cys Cys Val Pro Thr
358 305                      310                     315                     320
361 Ala Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile
362                      325                     330                     335

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374 <400> SEQUENCE: 5
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377 aggcattgcct ggtattgctg cctcctttca cactgcagtg ctcaatcttc tcaaggccaa      120
379 cacagctgca ggcaccactg gagggggctc atgctgtgta cccacggccc ggcgccccct      180
381 gtctctgctc tattatgaca gggacagcaa cattgtcaag actgacatac ctgacatggt      240
383 agtagaggcc tgtgggtgca gttag      265
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389 <213> ORGANISM: Homo sapiens
391 <400> SEQUENCE: 6
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396 cgagtccaca ccacccacc      139
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400 <211> LENGTH: 27
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429 <211> LENGTH: 10
430 <212> TYPE: PRT
431 <213> ORGANISM: Homo sapiens
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440 <211> LENGTH: 44
441 <212> TYPE: DNA

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